

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 13:55:36 ; Search time 58 Seconds
(without alignments)
6062.518 Million cell updates/sec

Title: US-09-936-024-2
Perfect score: 813
Sequence: 1 gttgagaaacaccaccta.....agcgttctccctgtgcac 813
Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 381593 seqs, 21625194 residues 763186
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	813	100.0	1077	10	US-09-935-727-1
2	813	100.0	1114	10	US-09-896-096A-2
3	813	100.0	1114	10	US-09-894-924-2
4	813	100.0	1347	10	US-09-877-156-18
5	809.4	99.6	1137	10	US-09-840-795-1
6	533.4	65.6	1859	10	US-09-877-156-19
7	515.4	63.4	903	10	US-09-935-727-32
8	473.4	58.2	491	10	US-09-896-096A-3
9	473.4	58.2	491	10	US-09-894-924-3
10	459	56.5	459	10	US-09-877-156-7
11	392.2	48.2	1550	10	US-09-935-727-33
12	387.4	47.7	1667	10	US-09-935-727-3
13	387	47.6	1796	10	US-09-935-727-28
14	245.2	30.2	271	10	US-09-896-096A-5
15	245.2	30.2	271	10	US-09-894-924-5
16	242.2	29.8	283	10	US-09-896-096A-10
17	242.2	29.8	283	10	US-09-894-924-10
18	220.8	27.2	499	10	US-09-935-727-17
19	218.8	26.9	226	10	US-09-896-096A-9

20	218.8	26.9	226	10	US-09-894-924-9	Sequence 9, Appli
21	200	24.6	201	10	US-09-896-096A-6	Sequence 6, Appli
22	200	24.6	201	10	US-09-894-924-6	Sequence 6, Appli
23	194.2	23.9	199	10	US-09-896-096A-8	Sequence 8, Appli
24	194.2	23.9	199	10	US-09-894-924-8	Sequence 8, Appli
25	183	22.5	233	9	US-09-292-758-141	Sequence 141, Appl
26	179	22.0	191	10	US-09-935-727-18	Sequence 18, Appl
27	152.2	18.7	277	10	US-09-896-096A-7	Sequence 7, Appli
28	152.2	18.7	277	10	US-09-894-924-7	Sequence 7, Appli
29	103.4	12.7	564	10	US-09-062-113-102	Sequence 102, App
30	103	12.7	594	10	US-09-062-113-97	Sequence 97, Appl
31	103	12.7	819	10	US-09-062-113-96	Sequence 96, Appl
32	103	12.7	966	10	US-09-062-113-101	Sequence 101, App
33	103	12.7	981	10	US-09-062-113-92	Sequence 92, Appl
34	103	12.7	984	10	US-09-062-113-93	Sequence 93, Appl
35	103	12.7	1056	10	US-09-062-113-95	Sequence 95, Appl
36	103	12.7	1089	10	US-09-062-113-10	Sequence 10, App
37	103	12.7	1182	10	US-09-062-113-100	Sequence 100, App
38	103	12.7	1200	10	US-09-062-113-94	Sequence 94, Appl
39	103	12.7	1203	12	US-10-105-934-3	Sequence 3, Appli
40	103	12.7	1206	10	US-09-062-113-6	Sequence 6, Appli
41	103	12.7	1206	10	US-09-062-113-83	Sequence 83, Appl
42	103	12.7	1206	10	US-09-062-113-84	Sequence 84, Appl
43	103	12.7	1206	10	US-09-062-113-85	Sequence 85, Appl
44	103	12.7	1206	10	US-09-062-113-86	Sequence 86, Appl
45	103	12.7	1206	10	US-09-062-113-87	Sequence 87, Appl

ALIGNMENTS

RESULT 1
US-09-935-727-1
; Sequence 1, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P2
; CURRENT APPLICATION NUMBER: US/09/935,727
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

LOCATION: (25)...(924)
US-09-935-727-1

Query Match 100.0%; Score 813; DB 10; Length 1077;
Best Local Similarity 100.0%; Pred. No. 7.8e-162; Indels 0; Gaps 0;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGCAGAAACACCACTACCTCCGCGGAGCGCAGAGACAGGGGAGCGCTGTGTGC 60
DB 112 GTGGCAGAAACACCACTACCTCCGCGGAGCGCAGAGACAGGGGAGCGCTGTGTGC 171

QY 61 GCCCAGTCCCCCAGGACCTTTGTGACAGCGCGCTGCGCGGAGCGCGCCGAGACAGCCACGAG 120
DB 172 GCCCAGTCCCCCAGGACCTTTGTGACAGCGCGCTGCGCGGAGCGCGCCGAGACAGCCACGAG 231

QY 121 TGTGCGCGCTGTCCACCGCGCACTACAGCAGTCTTGTGACACTCTGAGAGCGCTGTGCGGC 180
DB 232 TGTGCGCGCTGTCCACCGCGCACTACAGCAGTCTTGTGACACTCTGAGAGCGCTGTGCGGC 291

QY 181 TACTCAACGCTCTCTCCGCGGAGCGTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 240
DB 292 TACTCAACGCTCTCTCCGCGGAGCGTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 351

QY 241 AACCGTGTCTCGCGTCCGCGCACTCTTGTGACAGCGCTGTGAGAGCGCTGTGAGAGCAG 300
DB 352 AACCGTGTCTCGCGTCCGCGCACTCTTGTGACAGCGCTGTGAGAGCGCTGTGAGAGCAG 411

QY 301 GCATCGTGTCACTGTGTGCGCGGAGCGTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 360
DB 412 GCATCGTGTCACTGTGTGCGCGGAGCGTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 471

QY 361 TGCACAGCGCTGCGCGCGCGCGCACTCTTGTGACAGCGCTTGTGAGAGCGCTGTGAGAGCAG 420
DB 472 TGCACAGCGCTGCGCGCGCGCGCACTCTTGTGACAGCGCTTGTGAGAGCGCTGTGAGAGCAG 531

QY 421 CCCACACCGCACTGTGCGCGCGCGCGCACTCTTGTGACAGCGCTTGTGAGAGCGCTGTGAGAGCAG 480
DB 532 CCCACACCGCACTGTGCGCGCGCGCGCACTCTTGTGACAGCGCTTGTGAGAGCGCTGTGAGAGCAG 591

QY 481 GACACCGCTGTGCGCGCGCGCGCACTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 540
DB 592 GACACCGCTGTGCGCGCGCGCGCACTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 651

QY 541 GAGTGTGAGCGTGTGCGCGCGCGCGCACTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 600
DB 652 GAGTGTGAGCGTGTGCGCGCGCGCGCACTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 711

QY 601 CAGCGCGCTGTGCGCGCGCGCGCACTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 660
DB 712 CAGCGCGCTGTGCGCGCGCGCGCACTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 771

QY 661 CGCGCGCGCTGTGCGCGCGCGCGCACTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 720
DB 772 CGCGCGCGCTGTGCGCGCGCGCGCACTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 831

QY 721 GGGCGCGCTGTGCGCGCGCGCGCACTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 780
DB 832 GGGCGCGCTGTGCGCGCGCGCGCACTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 891

QY 781 CGGAGCGCTGTGAGCGCTTCTCCCTGTGCGAC 813
DB 892 CGGAGCGCTGTGAGCGCTTCTCCCTGTGCGAC 924

RESULT 2

US-09-936-096A-2
Sequence 2, Application US/09896096A
Patent No. US20020061559A1
GENERAL INFORMATION:
APPLICANT: ASHKENAZI, AVI J
APPLICANT: BOTSHEIN, DAVID
APPLICANT: DODGE, KELLY H.
APPLICANT: GURNEY, AUSTIN L.

APPLICANT: KIM, KYUNG JIN
APPLICANT: LAWRENCE, DAVID A.
APPLICANT: PITTI, ROBERT
APPLICANT: ROY, MARGARET A
APPLICANT: TURNER, DANIEL B
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: DCR3 Polypeptide, A TNFR Homolog
FILE REFERENCE: P1134R2 REVISED
CURRENT APPLICATION NUMBER: US/09/896,096A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 09/157,289
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: US 60/094,640
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 2
LENGTH: 1114
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Unsure
LOCATION: 1090
OTHER INFORMATION: Unknown base
US-09-896-096A-2

Query Match 100.0%; Score 813; DB 10; Length 1114;
Best Local Similarity 100.0%; Pred. No. 7.8e-162; Indels 0; Gaps 0;

Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGCAGAAACACCACTACCTCCGCGGAGCGCAGAGACAGGGGAGCGCTGTGTGC 60
DB 188 GTGGCAGAAACACCACTACCTCCGCGGAGCGCAGAGACAGGGGAGCGCTGTGTGC 247

QY 61 GCCCAGTCCCCCAGGACCTTTGTGACAGCGCGCTGCGCGGAGCGCGCCGAGACAGCCACGAG 120
DB 248 GCCCAGTCCCCCAGGACCTTTGTGACAGCGCGCTGCGCGGAGCGCGCCGAGACAGCCACGAG 307

QY 121 TGTGCGCGCTGTCCACCGCGCACTCTTGTGACAGCGCTTGTGAGAGCGCTGTGCGGC 180
DB 308 TGTGCGCGCTGTCCACCGCGCACTCTTGTGACAGCGCTTGTGAGAGCGCTGTGCGGC 367

QY 181 TACTCAACGCTCTCTCCGCGGAGCGTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 240
DB 368 TACTCAACGCTCTCTCCGCGGAGCGTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 427

QY 241 AACCGTGTCTCGCGTCCGCGCACTCTTGTGACAGCGCTTGTGAGAGCGCTGTGAGAGCAG 300
DB 428 AACCGTGTCTCGCGTCCGCGCACTCTTGTGACAGCGCTTGTGAGAGCGCTGTGAGAGCAG 487

QY 301 GCATCGTGTCACTGTGTGCGCGGAGCGTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 360
DB 488 GCATCGTGTCACTGTGTGCGCGGAGCGTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 547

QY 361 TGCACAGCGCTGCGCGCGCGCGCACTCTTGTGACAGCGCTTGTGAGAGCGCTGTGAGAGCAG 420
DB 548 TGCACAGCGCTGCGCGCGCGCGCACTCTTGTGACAGCGCTTGTGAGAGCGCTGTGAGAGCAG 607

QY 421 CCCACACCGCACTGTGCGCGCGCGCGCACTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 480
DB 608 CCCACACCGCACTGTGCGCGCGCGCGCACTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 667

QY 481 GACACCGCTGTGCGCGCGCGCGCACTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 540
DB 668 GACACCGCTGTGCGCGCGCGCGCACTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 727

QY 541 GAGTGTGAGCGTGTGCGCGCGCGCGCACTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 600
DB 728 GAGTGTGAGCGTGTGCGCGCGCGCGCACTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 787

QY 601 CAGCGCGCTGTGCGCGCGCGCGCACTGTGAGGAGGACAGGCTTGCACCGCCACCCAC 660

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 13:48:11 ; Search time 54 Seconds
(without alignments)
4617.189 Million cell updates/sec

Title: US-09-936-024-2

Perfect score: 813

Sequence: 1 gggcgagaaacacacaccta.....agcgcttctccctgtgcac 813

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/2/ina/5A COMB.seq:*
- 2: /cgn2_6/prodata/2/ina/5B COMB.seq:*
- 3: /cgn2_6/prodata/2/ina/6A COMB.seq:*
- 4: /cgn2_6/prodata/2/ina/6B COMB.seq:*
- 5: /cgn2_6/prodata/2/ina/6CTUS COMB.seq:*
- 6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	813	100.0	1164	2	US-08-794-796-1
2	813	100.0	1347	4	US-09-286-529-18
3	533.4	65.6	1859	4	US-09-286-529-19
4	459	56.5	459	4	US-09-286-529-7
5	129.6	15.9	525	3	US-08-997-918-47
6	112	13.8	2432	3	US-08-974-022-1
7	112	13.8	2432	4	US-08-795-445A-1
8	112	13.8	2432	4	US-08-795-447A-1
9	112	13.8	2432	4	US-08-794-186-1
10	112	13.8	2432	4	US-08-795-446B-1
11	112	13.8	2432	4	US-08-706-945D-123
12	110.4	13.6	1324	3	US-08-974-022-3
13	110.4	13.6	1324	4	US-08-795-445A-3
14	110.4	13.6	1324	4	US-08-795-447A-3
15	110.4	13.6	1324	4	US-08-974-186-3
16	110.4	13.6	1324	4	US-08-795-446B-3
17	110.4	13.6	1324	4	US-08-706-945D-125
18	103	12.7	1355	3	US-08-974-022-5
19	103	12.7	1355	4	US-08-795-445A-5
20	103	12.7	1355	4	US-08-795-447A-5
21	103	12.7	1355	4	US-08-974-186-5
22	103	12.7	1355	4	US-08-795-446B-5
23	103	12.7	1355	4	US-08-706-945D-127
24	76	9.3	3331	4	US-09-042-785A-1
25	68	8.4	76	4	US-09-042-785A-6
26	68	8.4	1815	4	US-09-042-785A-24
27	68	8.4	2185	3	US-08-959-382-1

28	68	8.4	2612	4	US-09-042-785A-3
29	68	8.4	2630	4	US-09-042-785A-22
30	68	8.4	3474	4	US-09-527-236A-1
31	56.4	6.9	1719	4	US-09-042-785A-5
32	54.8	6.7	1164	2	US-08-794-796-1
33	54.8	6.7	1347	4	US-08-286-529-18
34	52	6.4	2793	1	US-08-209-747-1
35	52	6.4	2793	2	US-08-458-298-1
36	51.6	6.3	3796	2	US-08-762-308-11
37	51.6	6.3	3796	4	US-08-844-634-10
38	51.6	6.3	3813	2	US-08-850-000-3
39	51.6	6.3	3813	6	5395760-3
40	49.6	6.1	691	1	US-08-266-080B-12
41	49.6	6.1	691	5	PCT-US95-05431-12
42	45.6	6.1	705	4	US-09-326-394-3
43	45.4	6.1	8906	2	US-08-826-267-1
44	48.6	6.0	1878	3	US-08-996-139-14
45	48.6	6.0	1878	4	US-08-995-659-14

ALIGNMENTS

RESULT 1
US-08-794-796-1
; Sequence 1, Application US/08794796
; Patent No. 5885800
; GENERAL INFORMATION:
; APPLICANT: Emery, John
; APPLICANT: Tan, KB
; APPLICANT: Truneh, Alem
; APPLICANT: Young, Peter
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,
; TITLE OF INVENTION: TR4
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,796
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: GH50000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1164 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLSCULE TYPE: cDNA
US-08-794-796-1

Query Match 100.0%; Score 813; DB 2; Length 1164;
Best Local Similarity 100.0%; Pred. No. 2.6e-154;

XX PA (ELIL) LILLY & CO ELI.
 XX PI Cohen FU, Posada JA, Wierda D;
 XX DR WPI; 2000-475441/41.
 XX DR P-PSDB; AA96596.
 XX PT Use of mature FLINT for treating e.g. acute respiratory distress
 XX PT syndrome, ulcerative colitis or ischemic injury during organ
 XX PS transplantation
 XX PS Example 7; Fig 1A-B, 125pp; English.
 XX CC Human FLINT (also known as osteoprotegerin 3) is a new tumour necrosis
 XX CC factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and
 XX CC prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas
 XX CC mediated apoptotic and pro-inflammatory activity. mFLINT is useful for
 XX CC treating acute respiratory distress syndrome, treating or inhibiting
 XX CC ulcerative colitis, inhibiting ischemic injury during organ
 XX CC transplantation or for organ preservation during transplantation. mFLINT
 XX CC can also be used to treat acute liver failure, inflammation of the liver,
 XX CC abnormal (hepatocyte) apoptosis, sepsis, disorders associated with
 XX CC inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,
 XX CC damage to a cardiac myocyte resulting from abnormal myocardial ischemia,
 XX CC Type I diabetes, cancer, damage to an innocent bystander tissue induced
 XX CC by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,
 XX CC myelodysplastic syndromes and pancytopenic conditions.
 XX SQ Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;
 Query Match 100.0%; Score 813; DB 21; Length 900;
 Best Local Similarity 100.0%; Pred. No. 5.1e-145;
 Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGCGAAGACCTCCATCCCTGCGCGGACGAGAGACGGGGAGCGGCTGTGTC 60
 Db 88 GTGGCGAAGACCTCCATCCCTGCGCGGACGAGAGACGGGGAGCGGCTGTGTC 147
 Qy 61 GCGCAGTGCCTTCTGGGGAGCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 120
 Db 148 GCGCAGTGCCTTCTGGGGAGCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 207
 Qy 121 TGTGGCGGCTTCCAGCGGCGCTACACGCGGTTCTGGAATCTGAGAGCGCTGCGC 180
 Db 208 TGTGGCGGCTTCCAGCGGCGCTACACGCGGTTCTGGAATCTGAGAGCGCTGCGC 267
 Qy 181 TACTCAGAGCTTCTTGGGGAGCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 240
 Db 268 TACTCAGAGCTTCTTGGGGAGCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 327
 Qy 241 AACCGTGCCTGCGGCGGCGGCGCTTCTGGGCGAGCGCTGTGAGAGAGAGAGAG 300
 Db 328 AACCGTGCCTGCGGCGGCGGCGCTTCTGGGCGAGCGCTGTGAGAGAGAGAGAG 387
 Qy 301 GATGTGTGCTACTGTGTGCGGCGGCTTCTGGGCGAGCGCTGTGAGAGAGAGAGAG 360
 Db 388 GCATGTGTGCTACTGTGTGCGGCGGCTTCTGGGCGAGCGCTGTGAGAGAGAGAGAG 447
 Qy 361 TGCAGAGCTGCGGCGGCGGCGGCTTCTGGGCGAGCGCTGTGAGAGAGAGAGAGAG 420
 Db 448 TGCAGAGCTGCGGCGGCGGCGGCTTCTGGGCGAGCGCTGTGAGAGAGAGAGAGAG 507
 Qy 421 CCCCAGCGAGCTGCGGCGGCGGCGGCTTCTGGGCGAGCGCTGTGAGAGAGAGAGAG 480
 Db 508 CCCCAGCGAGCTGCGGCGGCGGCGGCTTCTGGGCGAGCGCTGTGAGAGAGAGAGAG 567
 Qy 481 GACACCTGTGACAGCTGCTGCTTCTGGGCGAGCGCTGTGAGAGAGAGAGAGAGAG 540
 Db 568 GACACCTGTGACAGCTGCTGCTTCTGGGCGAGCGCTGTGAGAGAGAGAGAGAGAG 627
 Qy 541 GAGTGTGAGCTGCGGCGGCGGCGGCTTCTGGGCGAGCGCTGTGAGAGAGAGAGAG 600

Db 628 GAGTGTGAGCTGCGGCGGCGGCTTCTGGGCGAGCGCTGTGAGAGAGAGAGAG 687
 Qy 601 CAGCGGCTGCTGCGAGGCGGCTTCTGGGCGGAGCGGCTGTGAGAGAGAGAGAGAG 660
 Db 688 CAGCGGCTGCTGCGAGGCGGCTTCTGGGCGGAGCGGCTGTGAGAGAGAGAGAGAG 747
 Qy 661 CAGCGGCGCTTCTGAGCTGAGAGCTGCGGCGGCTTCTGGGCGGAGCGGCTGTGAGAGAGAGAGAG 720
 Db 748 CAGCGGCGCTTCTGAGCTGAGAGCTGCGGCGGCTTCTGGGCGGAGCGGCTGTGAGAGAGAGAGAG 807
 Qy 721 GAGGCGCTGCTGAGCTGAGAGCTGCGGCGGCTTCTGGGCGGAGCGGCTGTGAGAGAGAGAGAG 780
 Db 808 GAGGCGCTGCTGAGCTGAGAGCTGCGGCGGCTTCTGGGCGGAGCGGCTGTGAGAGAGAGAGAG 867
 Qy 781 CAGAGCGCTTCTGAGCGGCTTCTGCTTCTGCTGTCAC 813
 Db 868 CAGAGCGCTTCTGAGCGGCTTCTGCTTCTGCTGTCAC 900

RESULT 10
 AAX22300
 ID AAX22300 standard; DNA; 903 BP.
 XX AAX22300;
 AC AAX22300;
 XX XX
 DT 20-MAY-1999 (first entry)
 XX XX
 DE Orphan receptor (HUMAN NTR-1) polypeptide encoding DNA.
 XX XX
 KW HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human;
 KM tumour necrosis factor receptor; muscle disorder; bone mass; screening;
 XX muscle metabolism; binding agent; cognate ligand; ee.
 OS Homo sapiens.
 XX XX
 EN W09907738-A2.
 XX XX
 PD 18-FEB-1999.
 XX XX
 PF 04-AUG-1998; 98WO-US16202.
 XX XX
 PR 06-AUG-1997; 97US-0054869.
 XX XX
 PA (PROC) PROCTER & GAMBLE CO.
 PA (REGS-) REGENERON PHARM INC.
 XX XX
 PI Maslakowski PJ, Morris J, Valenzuela DM;
 XX XX
 DR WPI; 1999-167365/14.
 DR P-PSDB; AA95082.
 XX XX
 PT Novel orphan human receptor polypeptide and nucleic acid - useful as
 PT diagnostic reagents and for treatment of muscle disorders
 XX XX
 PS Claim 2; Page 21; 23pp; English.
 XX XX

This DNA encodes a HUMAN NTR-1 polypeptide, a novel orphan receptor. The protein is related to osteoprotegerin (OPG) and to tumour necrosis factor receptor (TNFR). Host cells transfected with a vector comprising the HUMAN NTR-1 nucleic acid are used for the recombinant expression of the protein. HUMAN NTR-1 proteins and antibodies immuno specific for the protein are useful for diagnosis and treatment of humans and animals, especially muscle disorders, as the receptor is involved in regulation of bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful for screening for novel binding agents, and cognate ligands, which may be used to treat disorders associated with HUMAN NTR-1 imbalance.

Sequence 903 BP; 129 A; 324 C; 305 G; 145 T; 0 other;
 Query Match 100.0%; Score 813; DB 20; Length 903;
 Best Local Similarity 100.0%; Pred. No. 5.1e-145;
 Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;